What is claimed is:

1. A method for indicating a correspondence between cDNA and genome sequences wherein the method comprises: locating a base position on a genome sequence to an axis 1 of a graph, and a base position on a cDNA sequence to another axis; and indicating by a segment on a graph a portion having a similarity of not less than a qualified ratio to the cDNA sequence, in a subsequence in the genome sequence having a base length of not less than a qualified base length.

2. The method for indicating the correspondence between cDNA and genome sequences of claim 1, wherein a plurality of cDNAs are located to a vertical axis and the corresponding relationships to the cDNAs are indicated using a different color for each cDNA.

3. A computer readable recording medium wherein a program is recorded which makes a computer execute the method for indicating the correspondence between cDNA and genome sequences, the method comprising the following steps of: inputting genome and cDNA sequences; searching a portion having a similarity of not less than a qualified ratio to the cDNA sequence, in a subsequence in the genome sequence having a base length of not less than a qualified base length; indicating the portion searched in the search step by a segment on a graph by locating the genome and cDNA sequences to vertical and horizontal axes or horizontal and vertical axes of the graph, respectively.

4. The recording medium of claim 3 wherein a program is recorded which makes a computer execute the method for indicating the correspondence between cDNA and genome sequences, the method further comprising a step of inputting the qualified base length and the qualified ratio of similarity.

5. A sequencer apparatus comprising means of: inputting a genome sequence by an access to a genome database connected to a network or to an internal database, and inputting a cDNA sequence obtained by sequencing; searching a portion having a similarity of not less than a qualified ratio to the cDNA sequence, in a subsequence in the genome sequence having a base length of not less than a qualified base length; indicating by a segment on a graph the portion searched in the above search step by locating the genome and cDNA sequences to vertical and

horizontal axes or horizontal and vertical axes of the graph, respectively, thereby indicating an exon-intron structure of a gene on the genome sequence corresponding to the cDNA sequence.

6. A method for designing primers comprising the following steps of: designing primer pairs in different exon regions holding an intron sequence between them, performing PCR by using the primers with genome and cDNA libraries, respectively; inputting genome and cDNA sequences amplified by the PCR step; searching a portion having the similarity of not less than a qualified ratio to the cDNA sequence, in a subsequence in the genome sequence having a base length of not less than a qualified base length; indicating the portion searched in the above search step by a segment on a graph by locating the genome and cDNA sequences to vertical and horizontal axes or horizontal and vertical axes of the graph, respectively, to show that a different polynucleotide has been amplified due to the presence of an intron sequence, thereby confirming the amplified genome sequence contains the intron sequence.